

SEQUENCE LISTING

<110> Harding, Robert Maxwell
Dale, James Langham
Becker, Douglas Keith
Hafner, Gregory John
Yang, Ilin

<120> Transcriptional Control Element, Chimeric Constructs and Uses

Therefor

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 attggctgcc tgaagctcgc agagatctt tgcaaattca actagccaaa gaaatcatcg 6840
 agaaggttcg tgaaaagctt cactctatct agataggatt ctgtgtgt gagtggcgca 6900
 ctgcgcata atgttagtaag gaattattgt acttttacgc tggacgccac taggctccat 6960
 gctttctgtat atgtcacatc acttttacga attgagcctc ggggagccgt tcgtacaaag 7020
 tagatgcttt tctagtcaca tctgactttt cttaaaagcag atgcccataa ctttattcga 7080
 gttgagcctc ggggagccgc tcgtttaaag atgctttt gaaaatgaca gcgcgtggtg 7140
 cgatgtcatt ctcacccctt cttaatgcg tcggccaccg actgcattat tgagattctc 7200
 ttatccctt gccacccat cgggtgcatt attgggattt cgtatcgagt cgagggacga 7260
 ggcctccact actccctataa aaggacctca acccctcaga agaacggcaa gccggaaaca 7320
 ccgaacttcc cattttctc ttgagtttt ccttgagct tgagcttgt tgtaatctt 7380
 catagtttct aagtctccga agaacgagca ccgtctcgta aaggagccga tcctttcca 7440
 accacacttt ttcttacct 7458

<210> 3
 <211> 146
 <212> PRT
 <213> Taro bacilliform virus

<400> 3

Met Ala Lys Lys Phe Glu Ala Ala Ile Lys Asp Trp Tyr Asp Asn Ser
1 5 10 15

Arg Arg Ala Asp Leu Ser Tyr Leu Asp Leu Ala Thr Thr Thr Lys Pro
20 25 30

Ser Ala Ser Gln Leu Ala His Asn Leu Gln Val Ile Phe Asp Arg Leu
35 40 45

Ser Leu His Ser Ser Val Ser Ile Lys Glu His Tyr Glu Val Val Ser
50 55 60

Lys Leu His Ser Leu Glu Lys Ser Ile Glu Glu Leu Lys Ser Glu Leu
65 70 75 80

Thr Thr Val Lys Arg Ala Leu Thr Ser Ile Gln Lys Glu Val Phe Thr
85 90 95

His Lys Pro Leu Thr Ala Gln Glu Val Gln Thr Leu Ala Gln Ser Leu
100 105 110

Ile Lys Glu Pro Lys Gln Ile Glu Gln Gln Ala Val Phe Leu Leu Lys
115 120 125

Glu Leu Lys Glu Gln Thr Ala Lys Ile Gln Ala Leu Leu His Glu Leu
130 135 140

Lys Ser
145

<210> 4
<211> 144
<212> PRT
<213> Taro bacilliform virus

<400> 4

Met Ser Val Pro Asn Ser Thr Tyr Pro Gly Tyr Ile Lys Ser Leu Glu
1 5 10 15

Glu Thr Lys Val Leu Gly Asp Pro Ser Val Gly Phe Ser Glu Ile Pro
20 25 30

Thr Thr Ala Ile Gly Thr Ala Thr Gly Phe Ser Thr Leu Tyr Lys Gln
35 40 45

Asn Asn Thr Ile Ile Asn Leu Leu Ile Ser Leu His Lys Lys Val Asp
50 55 60

Ser Leu Ser Lys Lys Thr Asp Val Asp Glu Leu Ala Thr Glu Leu Ser
65 70 75 80

Lys Leu Thr Ile Lys Asp Thr Pro Lys Val Lys Ala Lys Thr Pro Leu
85 90 95

Tyr Val Phe Lys Ser Pro Arg Leu Ile Leu Glu Glu Arg Tyr Lys
100 105 110

Ile Gly Leu Pro Pro Thr Thr Asp Trp Thr Trp Pro Val Gly His
115 120 125

Pro Phe Ala Pro Pro Lys Thr Ser Thr Lys Ala Ser Thr Ser Ser
130 135 140

<210> 5
<211> 1881
<212> PRT
<213> Taro bacilliform virus

<400> 5.

Met Ser Leu Ala Val Arg Asp Arg Gly Ser Asn Pro Ser Thr Ser Ser
1 5 10 15

Thr Val Pro Ser Gln Gln Asp Gln Ile Arg Asp Tyr Arg Asn Met Gln
20 25 30

Arg Val Arg His Thr Ala Glu Arg Ala Ala Arg Arg Ile Phe Pro Gly
35 40 45

Arg Phe Asn Arg Thr Leu Glu Ser Gln Ile Asn Pro Glu Ala Glu Ile
50 55 60

Arg Leu Ser Gln Gln Arg Arg Ala Ala Met Val Pro Ala Glu Val Leu
65 70 75 80

Tyr Asn Thr Ser Pro Ser Thr Arg Asn Gln Lys Val Tyr Gln His Tyr
85 90 95

Ser Glu Glu Arg Ile Leu Cys Thr Gly Gln Asn Gln Gln Leu Asn Leu
100 105 110

Pro Phe Ile Asn Glu Ser Ser Tyr Arg Ala Leu Arg Glu Ser Gly Gln
115 120 125

Gln His Leu His Ile Gly Leu Ile Met Ile Arg Val His Pro Leu His
130 135 140

Arg Arg Asn Ala Gly Thr Thr Ala Leu Ile Val Pro Arg Asp Ile Arg
145 150 155 160

Trp Asn Asp Asp Arg Ser Ile Ile Gly Thr Met Glu Ile Asp Leu Ser
165 170 175

Ala Gly Ser Gln Ile Val Tyr Ile Ala Pro Asn Ile Met Leu Ser Val
180 185 190

Glu Asp Phe Tyr Arg Asn Ile Gln Leu Ala Ile Gln Thr Gln Gly Tyr
195 200 205

Glu Asn Trp Asn Ser Ala Glu Ser Asn Leu Leu Ile Ser Arg Ala Leu
210 215 220

Ile Gly Arg Leu Thr Asn Asp Ser Phe Thr Gly Phe Gln Tyr Asn Ile
225 230 235 240

Ser Asn Val Ala Glu Tyr Leu His Ser His Gly Val Gln Ala Ile Glu
245 250 255

Gly Gln Ala His Pro Arg Thr Leu Gly Asn Arg Trp Ile Leu Gln Ala
260 265 270

Pro Ala Pro Pro Arg Ser Leu Val Pro Gln Asn Val Glu Thr Thr Thr
275 280 285

Leu Leu Asp Gly Asn Val Ser Ile Arg Phe Ser Asn Tyr His Gln Ala
290 295 300

Pro Val Asn Asp Thr Gln Asp Asn Ser His Pro Asp Ile Gln Glu Asp
305 310 315 320

Glu Asn Gln Phe Ile Gly Phe Leu Ser Asp Leu Gly Glu Glu Tyr Glu

325

330

335

Leu Glu Tyr Pro Ser Phe Thr Pro Val His Ala Asp Glu Phe Ile Phe
340 345 350

Ile Ile Ile Asn Gly Glu Glu Ile Pro Asp Asp Phe Val Ser Ser Phe
355 360 365

Cys Ser Asn Phe Ser Pro Pro Pro Ile Pro Glu Pro Glu Pro Thr Ala
370 375 380

Ile Glu Glu Thr Ala Phe Thr Leu Glu Glu Gln Phe Asn Asp Leu Asp
385 390 395 400

Tyr Pro Thr Leu Ile Ser Met Glu Lys Gln Leu Val Gln Ser Ser Val
405 410 415

Thr Ser Ala Tyr Asn Pro Pro Thr Glu Pro Leu Met Gly Gln Val Val
420 425 430

Tyr Pro Pro Ala Ser Ala Pro Arg Pro Gln Ala Glu Thr Ser Ser Thr
435 440 445

Ser Glu Arg Phe Lys Asn Phe Arg Ala Lys Pro Tyr Ser Thr Pro Thr
450 455 460

Ile Phe Leu Pro Pro Ala Tyr Asn Gln Gln Gly Ala Ile Leu Val Leu
465 470 475 480

Pro Asp Asp Ile Gly Leu Tyr Glu Asp Thr Ile Ser Arg Trp Glu Ser
485 490 495

Ile Thr Leu Asn Met Met Asn Glu Lys Val Trp Pro Ser Asn Glu Ala
500 505 510

Lys Ala Lys Tyr Met Glu Asn Leu Leu Gly Glu Met Glu Lys Lys Thr
515 520 525

Trp Ile Gln Trp Arg Thr Thr Tyr Val Ser Glu Tyr Asp Ala Leu Val
530 535 540

Gln Gln Ser Asp Glu Thr Gln Asn Leu Leu Ser Gln Val Arg Arg Ile
545 550 555 560

Phe Leu Leu Gln Asp Pro Tyr Gln Gly Ser Thr Ala Glu Gln Asp Gln
 565 570 575

Ala Tyr Asn Asp Leu Glu Arg Ile Ser Cys Asp Asn Ile Lys Asp Leu
580 585 590

Ile Pro Tyr Leu Ile Gln Phe Arg Asn Leu Ala Ala Lys Ser Gly Arg
595 600 605

Leu Phe Leu Gly Pro Glu Leu Ser Glu Lys Leu Phe Arg Lys Met Pro
610 615 620

Pro Leu Ile Gly Lys Glu Ile Glu Thr Ala Phe Ile Ala Lys His Gly
625 630 635 640

Asn Ala Asn Ile Thr Val Met Pro Arg Ile His Phe Ala Tyr His Tyr
645 650 655

Leu Ala Glu Leu Cys Lys Lys Ala Ala Leu Gln Arg Ser Leu Lys Asp
660 665 670

Leu Ser Phe Cys Asn Gln Ile Pro Leu Pro Gly Ile Tyr Thr Lys Gly
675 680 685

Asn Lys Lys Phe Gly Leu Arg Lys Ala Arg Thr Tyr Lys Gly Lys Pro
690 695 700

His Pro Thr His Val Arg Val Phe Lys Lys Ala Lys Tyr Gln Arg Thr
705 710 715 720

Lys Lys Cys Lys Cys Phe Ile Cys Gly Glu Pro Gly His Phe Ala Arg
725 730 735

Glu Cys Thr Lys Gln Arg Gly Asn Ile Val Arg Ala Thr Val His Gln
 740 745 750

Glu Leu Ala Ile Pro Asp Asn Phe Asp Val Val Ser Val Asp Ala Asp
755 760 765

Glu Ser Asp Ser Ser Gly Ile Tyr Ser Tyr Ser Glu Asn Glu Ala Pro
 770 775 780

Leu Gln Glu Val Asn Ser Phe Ile His Asp Glu Asn Ile Phe Phe Leu
785 790 795 800

Ser Asp Ala Asp Glu Phe Glu Ser Pro Gln Gln His Leu His Glu Thr
805 810 815

Val Asn Met Leu Gln Ser Arg Ser Ala Tyr Leu Pro Gln Val Ala Val
820 825 830

Gly Glu Glu Lys Leu Asn Cys Ser His Ile Trp Leu Gln Asp Val Asp
835 840 845

Ile Pro Ser Asp Lys His Lys Cys His Thr Cys Arg Arg Asp Thr Gln
850 855 860

Lys His Tyr Arg Leu Glu Cys Gln Lys Cys Lys Phe Leu Val Cys Ser
865 870 875 880

Leu Cys Thr Ile Pro Tyr Leu Gly Ile Thr Met Gln Phe Arg Gln Lys
885 890 895

Gln Lys Ser Gln Pro Glu Asn Pro Asn Leu Val Arg Glu Leu Leu Glu
900 905 910

His Ala Ile Phe Leu Glu Glu Lys Cys Lys Asn Gln Glu Leu Leu Ser
915 920 925

Glu Thr Gln Ile Glu Arg Ile Val Ser Ser Glu Lys Gln Val Lys Phe
930 935 940

Tyr Gly Ile Leu Pro Thr Lys Lys Ser Asn Lys Ser Ala Gly Tyr Asp
945 950 955 960

Leu Gln Ser Asn Ile Asp Ile Glu Ile Pro Pro Gly Lys Cys Thr Val
965 970 975

Ile Ser Thr Gly Thr Phe Leu Gln Met Pro Asp Asn Met Tyr Gly Arg
980 985 990

Leu Val Glu Arg Thr Ser Leu Ala Ile Gln Gly Ile Thr Val Gln Gly
995 1000 1005

Gly Val Ile Asp Pro Asp Phe Thr Gly Glu Ile Gln Ile Val Leu
 1010 1015 1020

Phe Asn His Asn Thr Ala Pro Tyr Pro Val Lys Lys Thr Tyr Arg
 1025 1030 1035

Leu Ala Gln Ile Ile Phe Glu Lys Phe Tyr Thr Pro Ile Phe Ile
 1040 1045 1050

Gln Glu Pro Phe Thr Ser Thr Gln Gln Gly Ser Ser Asn Phe Gly
 1055 1060 1065

Ser Thr Ala Lys Pro Leu Gln Ile Thr Glu Asn Ile Glu Val Met
 1070 1075 1080

Ser Glu Thr Val Ala Asn Gln Val Ala Lys Ser Ser Val Leu Pro
 1085 1090 1095

Arg Leu Tyr Ser Ile Gln Ala His Ile His Ile Ala Pro Asp Ile
 1100 1105 1110

Val Ile Ser Thr Thr Ala Ile Ile Asp Thr Gly Ala Thr Val Cys
 1115 1120 1125

Cys Ile Ser Glu Lys Ile Val Pro Glu Ala Ala Lys Glu Gln Leu
 1130 1135 1140

Asn Tyr Lys Val Asn Ile Ser Gly Ile Ser Ser Gln Gln Gln Ile
 1145 1150 1155

Gln His Arg Leu Lys Arg Gly Thr Leu Glu Ile Ala Ser Asn Lys
 1160 1165 1170

Tyr Ala Leu Pro Leu Cys Tyr Ile Ile Glu Leu Asn Asp Lys Asp
 1175 1180 1185

Asp Phe Ser Met Ile Leu Gly Cys Asn Phe Phe Lys His Met Gly
 1190 1195 1200

Gly Gly Met Arg Phe Glu Gly Pro His Val Thr Phe Tyr Lys Gly
 1205 1210 1215

Ile Thr Thr Leu Ser Thr Ser Tyr Ala Asn Thr Gly Ile Asp Thr

1220	1225	1230
Glu His Glu Gln Ile Thr Ser Thr Thr Ser Gln Ser Phe Lys Glu		
1235	1240	1245
Arg Phe Ser Pro Leu Met Asn Glu Leu Lys Ala Ala Gly Tyr Ile		
1250	1255	1260
Gly Glu Asp Pro Leu Lys His Trp Ser Lys Asn Lys Val Thr Cys		
1265	1270	1275
Lys Leu Asp Leu Lys Asn Thr Glu Ile Thr Ile Gln Asp Lys Pro		
1280	1285	1290
Leu Arg His Ile Thr Pro Ala Leu Glu Gln Ser Tyr Gly Arg His		
1295	1300	1305
Val Asn Ala Leu Leu Met Leu Lys Val Ile Gln Pro Ser Lys Ser		
1310	1315	1320
Arg His Arg Thr Met Ala Phe Leu Val Asn Ser Gly Thr Thr Val		
1325	1330	1335
Thr Ala Asp Gly Lys Glu Ile Lys Gly Lys Glu Arg Met Val Phe		
1340	1345	1350
Asn Tyr Lys Ala Leu Asn Asp Asn Thr Tyr Lys Asp Gln Tyr Ser		
1355	1360	1365
Leu Pro Asn Ile Gln Leu Ile Leu Lys Lys Val Ile Asn Ser Thr		
1370	1375	1380
Ile Tyr Ser Lys Phe Asp Leu Lys Ser Gly Phe His Gln Val Ala		
1385	1390	1395
Met Asp Pro Asp Ser Val Glu Trp Thr Ala Phe Leu Val Pro Gln		
1400	1405	1410
Gly Leu Tyr Glu Trp Leu Ala Met Pro Phe Gly Leu Lys Asn Ala		
1415	1420	1425
Pro Ala Val Phe Gln Arg Lys Met Asp Ala Val Phe Lys Gly Cys		
1430	1435	1440

Glu Lys Phe Leu Ala Val Tyr Ile Asp Asp Ile Leu Val Phe Ser
 1445 1450 1455

Asn Asn Glu Glu Asp His Ala Lys His Leu Val Ile Met Leu Gln
 1460 1465 1470

Arg Cys Lys Glu His Gly Leu Val Leu Ser Pro Thr Lys Met Asn
 1475 1480 1485

Ile Ala Val Arg Glu Val Asn Phe Leu Gly Ala Thr Ile Gly Ser
 1490 1495 1500

Arg Lys Val Lys Leu Gln Glu Asn Ile Ile Lys Lys Ile Leu Asp
 1505 1510 1515

Phe Asp Thr Glu Lys Leu Gln Ser Lys Lys Gly Leu Arg Ser Phe
 1520 1525 1530

Leu Gly Ile Leu Asn Tyr Ala Arg Asn His Ile Pro Asn Leu Gly
 1535 1540 1545

Lys Ile Ala Gly Pro Leu Tyr Ser Lys Thr Ser Ile Tyr Gly Asp
 1550 1555 1560

Ile Arg Phe Ser Ala Ser Asp Trp Lys Leu Ile Asn Glu Ile Lys
 1565 1570 1575

Ala Ile Val Glu Lys Leu Pro Pro Leu Asp Tyr Pro Pro Glu Gln
 1580 1585 1590

Ala Tyr Ile Ile Ile Glu Ser Asp Gly Cys Met Glu Gly Trp Gly
 1595 1600 1605

Ala Ile Cys Lys Trp Lys Leu Ala Glu Tyr Asp Pro Lys Ser Ser
 1610 1615 1620

Glu Gln Ile Cys Ala Tyr Ala Ser Gly Lys Phe Ser Pro Ile Lys
 1625 1630 1635

Ser Thr Ile Asp Ala Glu Ile Thr Ala Ala Met Glu Gly Leu Glu
 1640 1645 1650

Ala Phe Lys Ile His Tyr Leu Asp Lys Gln Lys Ile Thr Leu Arg
1655 1660 1665

Thr Asp Cys Gln Ala Ile Ile Ser Phe Cys Asn Lys Thr Ser Val
1670 1675 1680

Asn Lys Pro Ser Arg Val Arg Trp Leu Lys Phe Ile Asp Tyr Ile
1685 1690 1695

Thr Asn Thr Gly Ile Asp Val Lys Phe Glu His Ile Asp Ala Lys
1700 1705 1710

Asn Asn Val Leu Ala Asp Thr Leu Ser Arg Leu Val Asn Thr Leu
1715 1720 1725

Gln Asp Leu Pro Trp Leu Asp Glu Pro His Gln Asp Gln Thr Val
1730 1735 1740

Ser Leu Met Gln Glu Ile Glu Asp Ala Pro Leu Glu Ile Lys Gln
1745 1750 1755

Arg Ser Leu Thr Cys Leu Gln Arg Leu Ile Cys Arg Ser Phe Met
1760 1765 1770

Glu Asp Ser Thr Glu Glu Ala Ile His Phe Leu Glu Asp Asp Lys
1775 1780 1785

Ile Glu Pro Thr Ala Glu Ser Ser Thr Pro Ile Thr Leu Asp Glu
1790 1795 1800

Phe Ser Arg Lys Arg Phe Gln Glu His Thr Asp Leu Leu Glu Glu
1805 1810 1815

Phe Gln Leu Thr Leu Leu Gln Ile Asn Leu Leu Glu Ala Ser Leu
1820 1825 1830

His Glu Arg Leu Met Lys Cys Gln Ser Tyr Ala Thr Arg Asp Asn
1835 1840 1845

Phe Trp Gly Asp Trp Leu Pro Glu Ala Arg Arg Asp Leu Leu Gln
1850 1855 1860

Ile Gln Leu Ala Lys Glu Ile Ile Glu Lys Val Arg Glu Lys Leu
 1865 1870 1875

His Ser Ile
 1880

<210> 6
<211> 1190
<212> DNA
<213> Taro bacilliform virus

<400> 6
gccttcacgg gttagatgg tgaagttcat tgattatatt actaacactg gaattgatgt 60
taaatttcaa catattgatg ctaaaaataa tgtcttagct gacactctgt ccaggttagt
taaacacttg caggatttgc catggctaga tgaacctcat caggatcaaa cagtctccct 120
gatgcaggaa attgaagatg cacctcttga aatcaagcag cgttcttaa cctgcttaca
gagactgatc tgtagaagct tcatttgcaga ttctacagaa gaagcttattc acttcctcga 180
agatgataag atcgagccaa cagctgagtc atcaacccca attactttgg atgaattttc
aagaaaaaaga ttccaagaac atacagatct cttagaagaa tttcaattaa ctttgcttca 240
aattaatctt cttgaagcat ctcttcatga acgattaatg aaatgccaaa gttatgcaac
gagagataat ttctggggag attggctgcc tgaagctcgc agagatctt tgcaaattca 300
actagccaaa gaaatcatcg agaagggttcg tgaaaagctt cactctatct agataggatt
ctttgtgtgt gagtggcgca cttgcgcata atgttagtaag gaattattgt acttttacgc 360
tggacgcccac taggctccat gctttctgtatgtcacatc acttttacga attgagccctc
ggggagccgt tcgtacaaag tagatgttt tcttagtcaca tctgactttt ctAAAAGCAG 420
atgccatcaa ctttatttgc gttgagccctc ggggagccgc tcgtttaaag atgcttttt
gaaaatgaca gcgcgtggtg cgatgtcatt ctcacctttt cttaatgcg tggccaccg 480
actgcattat tgagattctc ttatcccttt gccacctcat cggttgcatt attgggattt
cgtatcgagt cgagggacga ggcctccact actcctataa aaggaccta acccctaaga 540
agaacggcaa gccggaaaca ccgaacttcc cattttctc ttgagttttt ctttgagct
tgagtttg tgtaatctt catagttct aagtctccga agaacgagca ccgtctcg 600
aaggagccga tcctttcca accacacttt ttctacctt gtatcagagc 660
1190

<210> 7
<211> 598

<212> DNA
<213> Taro bacilliform virus

<400> 7
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tttacgctg gacgccacta ggctccatgc tttctgtaat gtcacatcac tttacgaat 120
tgagcctcgg ggagccgttc gtacaaagta gatgctttc tagtcacatc tgactttct 180
aaaagcagat gccatcaact ttattcgagt tgagcctcgg ggagccgctc gttaaagat 240
gctctttga aaatgacagc gcgtggtgcg atgtcattct cacctttct ttaatgcgtc 300
ggccaccgac tgcattattg agattctctt atccctttgc cacctcatcg gttgcattat 360
tgggatttcg tatcgagtcg agggacgagg cctccactac tcctataaaa ggacctcaac 420
ccctcagaag aacggcaagc cgaaaaacacc gaacttccc ttcttctctt gagtctttcc 480
tttgagcttg agcttgtgtg taatctttca tagtttctaa gtctccgaag aacgagcacc 540
gtctcgtgaa ggagccgatc ctttccaac cacactttt ctaccttggt atcagagc 598

<210> 8
<211> 529
<212> DNA
<213> Taro bacilliform virus

<400> 8
ggacgccact aggctccatg ctttctgtaa tgcacatca ctttacgaa ttgagcctcg 60
gggagccgtt cgtacaaagt agatgctttt ctgtcacat ctgactttc taaaagcaga 120
tgccatcaac tttattcgag ttgagcctcg gggagccgct cgtttaaaga tgctctttg 180
aaaatgacag cgcgtggtgc gatgtcattc tcacctttc ttatgcgt cgccaccga 240
ctgcattatt gagattctct tatccctttg ccacctcatc gttgcatta ttgggatttc 300
gtatcgagtc gagggacgag gcctccacta ctccataaaa aggaccta cccctcagaa 360
gaacggcaag ccggaaacac cgaacttccc attcttctct tgagtctttc ctggagctt 420
gagcttgtgt gtaatctttc atagttctta agtctccgaa gaacgagcac cgtctcgtga 480
aggagccgat cttttccaa ccacactttt tctaccttggt tatcagagc 529

<210> 9
<211> 261
<212> DNA
<213> Taro bacilliform virus

<400> 9
tgccacctca tcggttgcat tattgggatt tcgtatcgag tcgagggacg aggccctccac 60

tactcctata aaaggacctc aacccttcag aagaacggca agccggaaac accgaacttc 120
ccattcttctt cttgagtctt tcctttgagc ttgagcttgt gtgtaatctt tcatagtttc 180
taagtctccg aagaacgagc accgtctcgtaaaggagccg atcctttcc aaccacactt 240
tttctacctt ggtatcagag c 261

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Badna FP primer

<220>
<221> modified_base
<222> (5)..(6)
<223> I

<220>
<221> modified_base
<222> (10)..(11)
<223> I

<220>
<221> modified_base
<222> (18)..(19)
<223> I

<400> 10
atgccttygg aaraaygcc 20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Badna RP primer

<220>
<221> modified_base
<222> (9)..(10)
<223> I

<220>
<221> modified_base
<222> (11)..(12)
<223> I

<220>
<221> modified_base
<222> (13)..(14)
<223> I

<220>
<221> modified_base
<222> (18)..(19)
<223> I

<400> 11
ccayttrcaa cscccccacc

20

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> 1F primer

<400> 12
ggatgcagta ttcaaagggt gtg

23

<210> 13
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> TRBR primer

<400> 13
ctgcaggcgg ccgcgcctcg atacca

26

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> 5F primer

<400> 14
agtctttcct ttgagcttga gc

22

<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> G2R primer

<400> 15
cacacccttt gaatactgca tccat 25

<210> 16
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Cytoplasmic initiator methionine tRNA (tRNAmet) binding site

<400> 16
tggtatcaga gc 12

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> F-GTN primer

<400> 17
ctgcagatag gatttttgt gtgtg 25

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> R-GTN primer

<400> 18
ccatgggctc tgataccaag gtag 24

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> P527-F primer

<400> 19
ctgcaggac gccactaggc 20

<210> 20
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> P257-F primer

<400> 20
ctgcaggcca cctcatcggt tgc 23

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> P114-F primer

<400> 21
ctgcaggagc ttgagcttgt gtg 23

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> FP-as-1 primer

<400> 22
ctgcaggcct tcacgggtta gatg 24

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> TRBR-Bam primer

<400> 23
ggatccgctc tgataccaaag gtag 24

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> FP-6765-pro primer

<400> 24
ctgcaggggg agattggctg c 21

<210> 25
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> P600Not-F primer

<400> 25
ggaagcttgc ggccggccgag aaggttcg 28

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> P600Bgl-R primer

<400> 26
gcggaagatc ttgctctgtat accaaggtag 30

<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> RP-leader primer

<400> 27
ccatggatca tataattgtt aggtcgc 27

<210> 28
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> GUS1 primer

<400> 28
atgtttacgt cctgt 15

<210> 29
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> GUS2 primer

<400> 29
ttacttggttt gc

12

27